



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 10/650,326A
Source: FWO
Date Processed by STIC: 4/26/04

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MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

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Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

3 <110> APPLICANT: CURIS INC. AND WASHINGTON UNIVERSITY
 5 <120> TITLE OF INVENTION: CONJOINT ADMINISTRATION OF MORPHOGENS AND ACE INHIBITORS IN
 6 TREATMENT OF CHRONIC RENAL FAILURE
 8 <130> FILE REFERENCE: JJJ-P01-599
 10 <140> CURRENT APPLICATION NUMBER: 10/650,326A
 11 <141> CURRENT FILING DATE: 2003-08-28
 13 <150> PRIOR APPLICATION NUMBER: 60/406,431
 14 <151> PRIOR FILING DATE: 2002-08-28
 16 <160> NUMBER OF SEQ ID NOS: 31
 18 <170> SOFTWARE: PatentIn version 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 139
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
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 32 20 25 30
 35 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
 36 35 40 45
 39 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
 40 50 55 60
 43 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
 44 65 70 75 80
 47 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
 48 85 90 95
 51 Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
 52 100 105 110
 55 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
 56 115 120 125
 59 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
 60 130 135
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 64 <211> LENGTH: 97
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Homo sapiens
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 71 1 5 10 15
 74 Leu Ser Ile Leu Gly Leu Pro His Arg Pro Arg Pro His Leu Gln Gly
 75 20 25 30
 78 Lys His Asn Ser Ala Pro Met Phe Met Leu Asp Leu Tyr Asn Ala Met

Does Not Comply
Corrected Diskette Needed

pp 6, 9, 11-14

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DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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82 Ala Val Glu Glu Gly Gly Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro
83      50          55          60
86 Tyr Lys Ala Val Phe Ser Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln
87 65          70          75          80
90 Asp Ser His Phe Leu Thr Asp Ala Asp Met Val Met Ser Phe Val Asn
91          85          90          95
94 Leu
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98 <211> LENGTH: 431
99 <212> TYPE: PRT
100 <213> ORGANISM: Homo sapiens
102 <400> SEQUENCE: 3
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108 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
109          20          25          30
112 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
113          35          40          45
116 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
117          50          55          60
120 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
121 65          70          75          80
124 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
125          85          90          95
128 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
129          100          105          110
132 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
133          115          120          125
136 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
137          130          135          140
140 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
141 145          150          155          160
144 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
145          165          170          175
148 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
149          180          185          190
152 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
153          195          200          205
156 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
157          210          215          220
160 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
161 225          230          235          240
164 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
165          245          250          255
168 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
169          260          265          270
172 Lys Gln Pro Phe Met Val Ala Phe Lys Ala Thr Glu Val His Phe
173          275          280          285

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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176 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
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180 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
181 305      310      315      320
184 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
185      325      330      335
188 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
189      340      345      350
192 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
193      355      360      365
196 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
197      370      375      380
200 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
201 385      390      395      400
204 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
205      405      410      415
208 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
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212 <210> SEQ ID NO: 4

213 <211> LENGTH: 139

214 <212> TYPE: PRT

215 <213> ORGANISM: Mus musculus

217 <400> SEQUENCE: 4

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223 Asn Gln Glu Ala Leu Arg Met Ala Ser Val Ala Glu Asn Ser Ser Ser
224      20      25      30
227 Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
228      35      40      45
231 Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
232      50      55      60
235 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
236 65      70      75      80
239 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro
240      85      90      95
243 Asp Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
244      100      105      110
247 Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
248      115      120      125
251 Arg Asn Met Val Val Arg Ala Cys Gly Cys His
252      130      135

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255 <210> SEQ ID NO: 5

256 <211> LENGTH: 139

257 <212> TYPE: PRT

258 <213> ORGANISM: Homo sapiens

260 <400> SEQUENCE: 5

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262 Ala Val Arg Pro Leu Arg Arg Arg Gln Pro Lys Lys Ser Asn Glu Leu
263 1      5      10      15
266 Pro Gln Ala Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His Gly Ser

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DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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267          20          25          30
270 His Gly Arg Gln Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln
271          35          40          45
274 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
275          50          55          60
278 Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn
279 65          70          75          80
282 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
283          85          90          95
286 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
287          100          105          110
290 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
291          115          120          125
294 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
295          130          135
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303 <400> SEQUENCE: 6
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306 1          5          10          15
309 Pro His Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
310          20          25          30
313 Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu Tyr Val Ser Phe Arg
314          35          40          45
317 Asp Leu Gly Trp Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala
318          50          55          60
321 Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp Ser Cys Met Asn
322 65          70          75          80
325 Ala Thr Asn His Ala Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
326          85          90          95
329 Asp Val Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr
330          100          105          110
333 Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His
334          115          120          125
337 Arg Asn Met Val Val Lys Ala Cys Gly Cys His
338          130          135
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342 <211> LENGTH: 588
343 <212> TYPE: PRT
344 <213> ORGANISM: Drosophila melanogaster
346 <400> SEQUENCE: 7
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349 1          5          10          15
352 Ile Val Arg Val Ala Ser Thr Glu Asp Ile Ser Gln Arg Phe Ile Ala
353          20          25          30
356 Ala Ile Ala Pro Val Ala Ala His Ile Pro Leu Ala Ser Ala Ser Gly
357          35          40          45

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RAW SEQUENCE LISTING

DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:48

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

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360 Ser Gly Ser Gly Arg Ser Gly Ser Arg Ser Gly Gly Ala Ser Thr Ser
361      50                      55                      60
364 Thr Ala Leu Ala Lys Ala Phe Asn Pro Phe Ser Glu Pro Ala Ser Phe
365 65                      70                      75                      80
368 Ser Asp Ser Asp Lys Ser His Arg Ser Lys Thr Asn Lys Lys Pro Ser
369                      85                      90                      95
372 Lys Ser Asp Ala Asn Arg Gln Phe Asn Glu Val His Lys Pro Arg Thr
373                      100                      105                      110
376 Asp Gln Leu Glu Asn Ser Lys Asn Met Ser Lys Gln Leu Val Asn Lys
377                      115                      120                      125
380 Pro Asn His Asn Lys Met Ala Val Lys Glu Gln Arg Ser His His Lys
381                      130                      135                      140
384 Lys Ser His His His Arg Ser His Gln Pro Lys Gln Ala Ser Ala Ser
385 145                      150                      155                      160
388 Thr Glu Ser His Gln Ser Ser Ser Ile Glu Ser Ile Phe Val Glu Glu
389                      165                      170                      175
392 Pro Thr Leu Val Leu Asp Arg Glu Val Ala Ser Ile Asn Val Pro Ala
393                      180                      185                      190
396 Asn Ala Lys Ala Ile Ile Ala Glu Gln Gly Pro Ser Thr Tyr Ser Lys
397                      195                      200                      205
400 Glu Ala Leu Ile Lys Asp Lys Leu Lys Pro Asp Pro Ser Thr Leu Val
401                      210                      215                      220
404 Glu Ile Glu Lys Ser Leu Leu Ser Leu Phe Asn Met Lys Arg Pro Pro
405 225                      230                      235                      240
408 Lys Ile Asp Arg Ser Lys Ile Ile Ile Pro Glu Pro Met Lys Lys Leu
409                      245                      250                      255
412 Tyr Ala Glu Ile Met Gly His Glu Leu Asp Ser Val Asn Ile Pro Lys
413                      260                      265                      270
416 Pro Gly Leu Leu Thr Lys Ser Ala Asn Thr Val Arg Ser Phe Thr His
417                      275                      280                      285
420 Lys Asp Ser Lys Ile Asp Asp Arg Phe Pro His His His Arg Phe Arg
421                      290                      295                      300
424 Leu His Phe Asp Val Lys Ser Ile Pro Ala Asp Glu Lys Leu Lys Ala
425 305                      310                      315                      320
428 Ala Glu Leu Gln Leu Thr Arg Asp Ala Leu Ser Gln Gln Val Val Ala
429                      325                      330                      335
432 Ser Arg Ser Ser Ala Asn Arg Thr Arg Tyr Gln Val Leu Val Tyr Asp
433                      340                      345                      350
436 Ile Thr Arg Val Gly Val Arg Gly Gln Arg Glu Pro Ser Tyr Leu Leu
437                      355                      360                      365
440 Leu Asp Thr Lys Thr Val Arg Leu Asn Ser Thr Asp Thr Val Ser Leu
441                      370                      375                      380
444 Asp Val Gln Pro Ala Val Asp Arg Trp Leu Ala Ser Pro Gln Arg Asn
445 385                      390                      395                      400
448 Tyr Gly Leu Leu Val Glu Val Arg Thr Val Arg Ser Leu Lys Pro Ala
449                      405                      410                      415
452 Pro His His His Val Arg Leu Arg Arg Ser Ala Asp Glu Ala His Glu
453                      420                      425                      430
456 Arg Trp Gln His Lys Gln Pro Leu Leu Phe Thr Tyr Thr Asp Asp Gly

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 <220> FEATURE:

This is not explained in <2207-2237
 section. See
 p. 14 for error
 explanation.

invalid. Do you mean Tyr?

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<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (82)..(82)
<223> OTHER INFORMATION: Xaa is Ile, Val or Asn
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: Xaa is Lys or Arg
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (85)..(85)
<223> OTHER INFORMATION: Xaa is Lys, Asn, Gln, His, Arg or Val
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (86)..(86)
<223> OTHER INFORMATION: Xaa is Tyr, Glu or His
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (87)..(87)
<223> OTHER INFORMATION: Xaa is Arg, Gln, Glu or Pro
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (88)..(88)
<223> OTHER INFORMATION: Xaa is Asn, Glu, Trp or Asp
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (90)..(90)
<223> OTHER INFORMATION: Xaa is Val, thr, Ala or Ile
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (92)..(92)
<223> OTHER INFORMATION: Xaa is Arg, Lys, Val, Asp, Gln or Glu

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<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (93)..(93)
<223> OTHER INFORMATION: Xaa is Ala, Gly, Glu or Ser
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (95)..(95)
<223> OTHER INFORMATION: Xaa is Gly or Ala
<220> FEATURE:
<221> NAME/KEY: Variant
<222> LOCATION: (97)..(97)
<223> OTHER INFORMATION: Xaa is His or Arg
<400> SEQUENCE: 24
Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
50 55 60
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa
65 70 75 80
Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
85 90 95
Xaa

same type error in sequences 25-30
Sequences 25 through 30 have Xaa's
explained, but not "Artificial Sequence".

see p. 12

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<210> SEQ ID NO 31

<211> LENGTH: 4

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: :

<400> SEQUENCE: 31

Gly Gly Pro Pro

1

*needs explanation in L2207-L2237
section*

This appeared several times in
sequences 28 and 29

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<220> FEATURE:

<221> NAME/KEY: VARIANT

<222> LOCATION: (46)...(46)

<223> OTHER INFORMATION: Xaa is (Asn, Lys, Val, Thr or Gln)?

also, several locations for
Xaa showed "Serj" as an
amino acid represented by

Xaa (on 2237 line)

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/650,326A

DATE: 04/26/2004
TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\04122004\J650326A.raw

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; Xaa Pos. 2,3,4,6,7,8,11,12,13,14,15,16,18,19,20,21,23,26,28,30,31
Seq#:24; Xaa Pos. 33,34,35,36,37,38,39,40,44,45,46,47,48,49,50,51,52,53,54
Seq#:24; Xaa Pos. 55,56,57,58,59,60,63,65,66,67,68,69,70,71,72,74,75,76,77
Seq#:24; Xaa Pos. 78,79,80,82,84,85,86,87,88,90,92,93,95,97
Seq#:25; Xaa Pos. 2,3,4,5,7,8,9,11,12,13,16,17,18,19,20,21,23,24,25,26,28
Seq#:25; Xaa Pos. 31,33,35,36,38,39,40,41,42,43,44,45,49,50,51,52,53,54,55
Seq#:25; Xaa Pos. 56,57,58,59,60,61,62,63,64,65,68,70,71,72,73,74,75,76,77
Seq#:25; Xaa Pos. 79,80,81,82,83,84,85,87,89,90,91,92,93,95,97,98,100,102
Seq#:26; Xaa Pos. 2,3,4,5
Seq#:27; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,18,19,20,21,22,23
Seq#:27; Xaa Pos. 24,26,28,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45
Seq#:27; Xaa Pos. 46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,63,65,66
Seq#:27; Xaa Pos. 67,68,69,70,71,72,74,75,76,77,78,79,80,81,82,83,84,85,86
Seq#:27; Xaa Pos. 87,88,89,90,91,92,93,95,97
Seq#:28; Xaa Pos. 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,23,24
Seq#:28; Xaa Pos. 25,26,27,28,29,31,33,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:28; Xaa Pos. 47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
Seq#:28; Xaa Pos. 66,68,70,71,72,73,74,75,76,77,79,80,81,82,83,84,85,86,87
Seq#:28; Xaa Pos. 88,89,90,91,92,93,94,95,96,97,98,100,102
Seq#:29; Xaa Pos. 2,3,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
Seq#:29; Xaa Pos. 75,80,82,84,89,96
Seq#:30; Xaa Pos. 2,3

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:24,25,26,27,28,29,30,31

Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec.1.823 of new Rules)

Seq#:28,29,31,24,25,26,27,30

VERIFICATION SUMMARY

DATE: 04/26/2004

PATENT APPLICATION: US/10/650,326A

TIME: 09:51:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04122004\J650326A.raw

L:2438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24
L:2838 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25
L:2893 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:3345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
M:341 Repeated in SeqNo=27
L:3380 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3712 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3828 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:28
L:3830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:4008 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:4010 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0
M:341 Repeated in SeqNo=29
L:4051 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:4060 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial
L:4060 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:4060